INPUT SET: S8120.raw

```
357   Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
358           1185             1190             1195
359
360   Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
361           1200             1205             1210
362
363   Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
364           1215             1220
365
366   Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
367   1225             1230             1235
368
369   Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
370       1240             1245             1250
371
372   Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
373           1255             1260             1265
374
375   Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
376           1270             1275             1280
377
378   Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
379               1285             1290
380
381   Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
382   1295             1300             1305
383
384   Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
385       1310             1315             1320
386
387   Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
388           1325             1330             1335
389
390   Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
391               1340             1345             1350
392
393   Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
394               1355             1360
395
396   Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
397   1365             1370             1375
398
399   Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
400       1380             1385             1390
401
402   Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
403           1395             1400             1405
404
405   Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
406           1410             1415             1420
407
408   Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
409               1425             1430
```

```
410
411    Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
412    1435                1440                1445
413
414    Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
415        1450                1455                1460
416
417    Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
418            1465                1470                1475
419
420    Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
421            1480                1485                1490
422
423    Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
424                1495                1500
425
426    Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
427    1505                1510                1515
428
429    Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
430        1520                1525                1530
431
432    Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
433            1535                1540                1545
434
435    Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
436                1550                1555                1560
437
438    Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
439                1565                1570
440
441    Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
442    1575                1580                1585
443
444    Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
445        1590                1595                1600
446
447    Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
448            1605                1610                1615
449
450    Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
451                1620                1625                1630
452
453    Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
454                1635                1640
455
456    Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
457    1645                1650                1655
458
459
460
```

2493   (2) INFORMATION FOR SEQ ID NO:19:

INPUT SET: S8120.raw

```
2494              (i) SEQUENCE CHARACTERISTICS:
-->  2495                (A) LENGTH:  813 base pairs      only 783 are
     2496                (B) TYPE:  Nucleic Acid                shown.
     2497                (C) STRANDEDNESS:  Double
     2498                (D) TOPOLOGY:  linear
     2499          (ii) MOLECULE TYPE:  Other nucleic acid
     2500                (A) DESCRIPTION: N19/8 scFv (His Tagged)
     2501
     2502
     2503   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:19:
     2504
     2505   ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30
     2506   Met Ala Asn Ile Val Leu Thr Gln Ser Pro
     2507    1               5                   10
     2508
     2509   GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60
     2510   Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
     2511                   15                  20
     2512
-->  2513   GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 120  90?,
     2514   Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
     2515                   25                  30
     2516
     2517   GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150 ?
     2518   Val Asp Ser Tyr Asp Asn Ser Phe Met His
     2519                   35                  40
     2520
     2521   TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180 ?
     2522   Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
     2523                   45                  50
     2524
     2525   AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210
     2526   Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu
     2527                   55                  60
     2528
     2529   GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240
     2530   Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
     2531                   65                  70
     2532
     2533   AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270
     2534   Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr
     2535                   75                  80
     2536
     2537   ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300
     2538   Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
     2539                   85                  90
     2540
     2541   ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330
     2542   Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val
     2543                   95                  100
     2544
     2545   CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360
     2546   Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu
```

INPUT SET: S8120.raw

```
2547                    105                 110
2548
2549   GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390
2550   Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser
2551                    115                 120
2552
2553   GGT GGC GGG GGA TCG GGT GGC GGA GGG TCG 420
2554   Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
2555                    125                 130
2556
2557   GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
2558   Asp Val Lys Leu Val Glu Ser Gly Gly Asp
2559                    135                 140
2560
2561   TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
2562   Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
2563                    145                 150
2564
2565   TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
2566   Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
2567                    155                 160
2568
2569   AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
2570   Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
2571                    165                 170
2572
2573   TCA GAG AAG AGG CTG GAG TTG GTC GCA GCC 570
2574   Ser Glu Lys Arg Leu Glu Leu Val Ala Ala
2575                    175                 180
2576
2577   ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
2578   Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
2579                    185                 190
2580
2581   CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
2582   Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
2583                    195                 200
2584
2585   TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
2586   Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
2587                    205                 210
2588
2589   CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690
2590   Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
2591                    215                 220
2592
2593   ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720
2594   Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr
2595                    225                 230
2596
2597   TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750
2598   Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp
2599                    235                 240
```

INPUT SET: S8120.raw

```
2600
2601   GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780
2602   Val Trp Gly Thr Gly Thr Thr Val Thr Val
2603                   245                 250
2604
2605   TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810
2606   Ser Ser Leu Glu His His His His His His
2607                   255                 260
2608
2609   TGA                                     813
2610
2611
2612
```

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR.18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested in the following locations:
1) Dial-up access to the Patent and Trademark Office Bulletin Board System.
   Phone number: 703-305-8950
   Cost: Free-of-charge
2) Dial-up access through the Internet. FTP site: ftp.uspto.gov
   Login as "anonymous". Software is in directory /pub/checker
   Cost: Free-of-charge
3) For diskette copies, telephone requests to 703-308-0322.
   Cost: $25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.